

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 149.542 Seconds
(without alignments)
1349.183 Million cell updates/sec

Title: US-09-939-537-29_COPY_1_394
Perfect score: 2029
Sequence: 1 MNRGVPPFRHLILVQLALLP.....SGOVLLENSNIKVLPWTSTPV 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:
1: uniprot_sprot:
2: uniprot_trembl:
2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2015	99.3	458	1 CD4_HUMAN
2	1991	98.1	458	1 CD4_PANTU
3	1844	90.9	458	1 CD4_MACFTU
4	1843	90.8	458	1 CD4_MACMUTU
5	1840	90.7	458	1 CD4_MACPA
6	1835	90.4	458	1 CD4_MACNE
7	1818	89.6	458	1 CD4_CERPE
8	1717	84.6	397	1 CD4_ERIFPA
9	1707	84.1	397	1 CD4_CERTO
10	1705	84.0	397	2 009261
11	1701	83.8	397	2 009260
12	1700	83.8	397	2 095NE9
13	1696	83.6	397	2 009259
14	1696	83.6	397	2 009263
15	1689	83.2	397	2 009262
16	1601.5	78.9	457	2 Q8HZT8
17	1575.5	77.6	457	2 Q8HZT7
18	1572.5	77.5	457	1 CD4_SAISC
19	1183.5	58.3	455	2 Q9XST8
20	1182.5	58.3	455	2 Q11QE2
21	1146	56.5	463	1 CD4_RAB17
22	1135	55.9	463	1 CD4_CANFA
23	1119.5	55.4	457	1 CD4_MOUSE
24	1099	54.2	432	2 Q61BK3
25	1097.5	54.1	447	2 Q6R3N4
26	1087	53.6	474	2 P79355
27	1078.5	53.6	466	2 Q6R3N3
28	999	49.2	457	1 CD4_RAT
29	983	48.9	457	1 CD4_MOUSE
30	985	48.5	457	2 Q61396
31	954.5	433	2 055054	mus musculu

32 400 19.7 86 2 077596
33 400 19.7 86 2 077597
34 398 19.6 86 2 061CP8
35 397 19.6 86 2 077594
36 397 19.6 86 2 077599
37 395 19.5 86 2 077595
38 395 19.5 86 2 071USS
39 392 19.3 86 2 077598
40 388 19.1 86 2 077601
41 383 18.9 86 2 077600
42 357 17.6 71 2 013969
43 305.5 15.1 99 2 029027
44 280.5 13.8 99 2 029028
45 271.5 13.4 482 2 Q90wbs

ALIGNMENTS

077596 mandrillus
077597 mandrillus
061CP8 homo sapien
077594 cercopithec
077599 theropithec
077595 cercopithec
071USS cercocebus
077598 papio sp. (c
077601 lophocebus
077600 lophocebus
013969 homo sapien
029027 sus scrofa
029028 sus scrofa
Q90wbs anas platyrhynchos

RESULT 1	CD4_HUMAN	STANDARD;	PRT;	458 AA.
ID	CD4_HUMAN			
AC	P01750;			
DT	01-NOV-1986 (Rel. 01, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Len-3).			
DE	Name=CD4;			
GN	Homo sapiens (Human),			
OC	Bukarjota, Metzcoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TAXID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	"The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family.", Cell 42:93-104(1985).			
RN	[2]			
RP	REVISION TO 26.			
RX	MEDLINE=89028655; PubMed=3262113; DOI=10.1016/0092-8674(88)90211-5;			
RA	Littman D.R., Madden P.J., Axel R.;			
RA	"Corrected CD4 sequence.", Cell 55:541-541(1988).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96303695; PubMed=8723724;			
RA	Ansari-Lari M.A., Mizny D.M., Lu J., Lu F., Lille C.E., Spanos S., Malley T., Gibbs R.A.;			
RA	"A gene-rich cluster between the CD4 and triosephosphate isomerase genes at human chromosome 12p13.1"; Genome Res. 6:314-326 (1996).			
RL	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT TRP-265.			
RX	MEDLINE=91216786; PubMed=1708753; DOI=10.1016/0198-8859(91)90077-M;			
RA	Hodge T.W., Sabo D.R., McDougal J.S.;			
RA	"Humans with OKT4 epitope deficiency have a single nucleotide base change in the CD4 gene, resulting in substitution of TRP240 for ARG240.", Hum. Immunol. 30:99-104(1991).			
RL	[5]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Pancreas; MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242608999;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruska K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Schuetz T.B., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,
 RA Richard S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzakwinski M.I., Skalska U., Smailus D.E.,
 RA Schmehl A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE OF 28-424 FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=91049640; PubMed=1425921;
 RA Pøringaard A., Hirsch V.M., Johnson P.R.;
 RT "Cloning and sequences of primate CD4 molecules: diversity of the
 RT cellular receptor for simian immunodeficiency virus/human
 RT immunodeficiency virus";
 RL Eur. J. Immunol. 22:2973-2981(1992).
 RN [7]
 RP SEQUENCE OF 26-394, AND DISULFIDE BOND.
 RX MEDLINE=90078222; PubMed=259274;
 RA Carr S.A., Hemling M.E., Folena-Wasserman G., Sweet R.W., Arumula K.,
 RA Barr J.R., Huddleston M.J., Taylor P.;
 RT "Protein and carbohydrate structural analysis of a recombinant soluble
 RT CD4 receptor by mass spectrometry";
 RL J. Biol. Chem. 264:21286-21295(1989).
 RN [8]
 RP SEQUENCE OF 26-40.
 RX MEDLINE=15340161; DOI=10.1101/pb.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites";
 RL Protein Sci. 13:2819-2824(2004).
 RN [9]
 RP REMOVAL FROM CELL SURFACE BY HIV-1 NEF, AND MUTAGENESIS OF MET-432;
 RP SER-433, 438-LEU-LEU-439 AND SER-440.
 RX PubMed=8124721;
 RA Aiken C., Konner J., Landau N.R., Lenburg M.E., Trono D.,
 RT "Net induces CD4 endocytosis: requirement for a critical dileucine
 RT motif in the membrane-proximal CD4 cytoplasmic domain";
 RL Cell 76:853-864(1994).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 26-208.
 RX MEDLINE=90611881; PubMed=170100; DOI=10.1038/34811a0;
 RA Wang J., Yan Y., Garrett T.P., Liu J., Rodgers D.W., Garlick R.L.,
 RA Marr G.E., Husain Y., Reinherz E.L., Harrison S.C.;
 RT "Atomic structure of a fragment of human CD4 containing two
 RT immunoglobulin-like domains";
 RL Nature 348:411-418(1990).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-208.
 RX MEDLINE=91251182; PubMed=2247146; DOI=10.1038/34819a0;
 RA Ryu S.-E., Kwong P.D., Truneh A., Porter T.G., Artios J.,
 RA Rosenberg M., Dai X., Xuong N.-H., Axel R., Sweet R.W.,
 RA Hendrickson W.A.;
 RT "Crystal structure of an HIV-binding recombinant fragment of human
 RT CD4. ";
 RL Nature 348:419-426(1990).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (3.9 ANGSTROMS) OF 26-388.
 RX MEDLINE=97311402; PubMed=9168119;
 RA Wu H., Kwong P.D., Hendrickson W.A.;
 RT "Dimeric association and segmental variability in the structure of
 RT human CD4";
 RL Nature 387:527-530(1997).
 RN [13]
 RP PALMITOYLATION.
 RX MEDLINE=92317088; PubMed=1618861;
 RA Crise B., Rose J.K.;
 RT "Identification of palmitoylation sites on CD4, the human
 RT immunodeficiency virus receptor";
 RL J. Biol. Chem. 267:13593-13597(1992).
 CC -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
 receptor interaction. May regulate T-cell activation.
 CC -!- SUBUNIT: Associates with p6-lck.
 CC -!- SUBUNIT LOCATION: Type I membrane protein. Removed from plasma
 membrane by HIV-1 Nef protein that increases clathrin-dependent
 endocytosis of this antigen to target it to lysosomal degradation.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD4 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd4.htm".
 CC -----
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 CC -----
 DR EMBL; M12807; AAA35572.1; --.
 DR EMBL; U07924; AAB81309.1; --.
 DR EMBL; BC025782; AAH25782.1; --.
 DR PIR; A900572; RWHTU4.
 DR PDB; 1CDH; X-ray; @=26-203.
 DR PDB; 1CDI; X-ray; @=25-203.
 DR PDB; 1CDJ; X-ray; @=26-203.
 DR PDB; 1CDU; X-ray; @=26-203.
 DR PDB; 1CDY; X-ray; @=26-203.
 DR PDB; 1WQ; X-ray; C=26-210.
 DR PDB; 1G9M; X-ray; C=26-210.
 DR PDB; 1GCI; X-ray; C=26-210.
 DR PDB; 1J4A; X-ray; D=26-203.
 DR PDB; 1Q68; NMR; A=421-458.
 DR PDB; 1WBR; NMR; @=427-445.
 DR PDB; 1WIO; X-ray; A/B=26-388.
 DR PDB; 1WIP; X-ray; A/B=26-388.
 DR PDB; 1WQ; X-ray; A/B=26-388.
 DR PDB; 3CD4; X-ray; @=26-207.
 DR GlycoSulitedB; P01730; --.
 DR Genew; HMG:1678
 DR H-InvDB; HIX0023001; --.
 DR MIM; 186940; --.
 DR GO; GO:0005886; C: plasma membrane; TAS.
 DR GO; GO:0005886; C: T-cell receptor complex; NAS.
 DR GO; GO:0042101; C: T-cell receptor activity; NAS.
 DR GO; GO:0015026; F: coreceptor activity; NAS.
 DR GO; GO:0015029; F: internalization receptor activity; TAS.
 DR GO; GO:004229; F: MHC class II protein binding; NAS.
 DR GO; GO:0004888; F: transmembrane receptor activity; TAS.
 DR GO; GO:0006955; F: immune response; NAS.
 DR GO; GO:0045086; P: positive regulation of interleukin-2 biosyn. . .; NAS.
 DR GO; GO:0030217; P: T-cell differentiation; NAS.
 DR GO; GO:0045058; P: T-cell selection; NAS.
 DR GO; GO:0007159; P: transmembrane receptor protein tyrosine kin. . .; NAS.
 DR InterPro; IPR008424; CD2.
 DR InterPro; IPR000973; CD4 TCAG.
 DR InterPro; IPR007110; Ig-Tike.
 DR InterPro; IPR003596; Ig-V.
 DR pfam; PF00047; Ig; 2.
 DR PRINTS; PR00692; CD4TCANTIGEN.
 DR SMART; SM00406; IgV; 1.
 DR PROST; PS50825; Ig; LIKE; 1.
 DR 3D-structure; Direct protein sequencing; Glycoprotein; Palmitate;
 KW Immune response; Immunoglobulin domain; Lipoprotein; Palmitate;
 KW Polymorphism; Repeat; Signal; T-cell; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 458
 FT DOMAIN 26 396
 FT TRANSM 397 418
 FT DOMAIN 419 458
 CYTOSLIC (Potential).

Db	241	QAERRASSKSWITFDLKNEKVSVKRVTDPLKQMGKKLPLHILTLPOALPOAGSGNITLA	300	FT DOMAIN 318 374	IG-like C2-type 3.
Db	301	LEAKYGKLOEVLVNVYMRATOLQNLTCWVGPSPKMLSLKLENKEAKVSKREKPVW	360	FT CARBOHYD 42 42	N-linked (GlcNAc. . .) (Potential).
Db	361	LNPEAGMWCQCLSDSGQVILLESNIKVLPLTWSTPV	394	FT CARBOHYD 296 296	N-linked (GlcNAc. . .) (By similarity).
Db	361	LNPEAGMWCQCLSDSGQVILLESNIKVLPLTWSTPV	394	FT DISULFID 325 325	N-linked (GlcNAc. . .) (By similarity).
RESULT 3				FT DISULFID 41 109	By similarity.
CD4_MACFU				FT DISULFID 155 184	By similarity.
ID CD4_MACFU		STANDARD;	PRT; 458 AA.	FT DISULFID 328 370	By similarity.
AC P79194;				FT LIPID 419 419	S-palmitoyl cysteine (By similarity).
DT 15-JUL-1998 (Rel. 36, Created)				FT LIPID 422 422	S-palmitoyl cysteine (By similarity).
DT 05-JUL-2004 (Rel. 44, Last annotation update)				FT SEQ 458 AA; 50828 MW; 7683E7E08105535 CRC64;	
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen					
DE T4/Leu-3)					
GN Name=CD4;					
OS Macaca fuscata fuscata (Japanese macaque)					
OC Macakoya; Metzcoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Cercopithecoidea; Macacinae; Macaca.					
NCBI TAXID=9543;					
RN [1]					
RP					
RA Hashimoto O., Tatsumi M.;					
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.					
CC -I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.					
CC -I- SUBUNIT: Associates with p56-1ck (By similarity).					
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.					
CC -I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.					
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CC					
CC DR EMBI; D63348; BAA09672.1; - .					
CC DR HSSP; P01730; 1WBR.					
CC DR GO:0042101; C-T-cell receptor complex; ISS.					
CC DR GO:0015026; P-coreceptor activity; ISS.					
CC DR GO:0042285; F:MH class II protein binding; ISS.					
CC DR GO:0006935; P-immune response; ISS.					
CC DR GO:0045085; P-positive regulation of interleukin-2 biosyn. . .; ISS.					
CC DR GO:00320217; P:T-cell differentiation; ISS.					
CC DR GO:0045058; P:T-cell selection; ISS.					
CC DR GO:0007169; P-transmembrane receptor protein tyrosine kin. . .; ISS.					
CC DR InterPro; IPR008424; CD4_TCag.					
CC DR InterPro; IPR00977; CD4.					
CC DR InterPro; IPR00710; Ig-like.					
CC DR InterPro; IPR03595; Ig_v.					
CC DR Pfam; PF00047; Ig; 2.					
CC PRINTS; PR00062; CD4ANTIGEN.					
CC DR SMART; SM00405; IgV_1.					
CC DR PROSITE; PS50835; Ig_LIKE; 1.					
CC KW Glycoprotein; Immune response; Lipoprotein;					
CC KW Palmitate; Repeat; Signal; T-cell; Transmembrane.					
CC SIGNAL 1 25					
CC By similarity.					
CC T-cell surface glycoprotein CD4.					
CC DOMAIN 26 458					
CC DOMAIN 26 396					
CC DOMAIN 397 418					
CC DOMAIN 419 458					
CC DOMAIN 26 125					
CC DOMAIN 126 203					
CC DOMAIN 204 317					
CC Ig-like C2-type 2.					
RESULT 4					
CD4_MACMU		STANDARD;	PRT; 458 AA.		
ID CD4_MACMU					
AC P16003; Q29617;					
DT 01-APR-1990 (Rel. 14, Created)					
DT 28-FEB-2003 (Rel. 41, Last sequence update)					
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen					
DE T4/Leu-3).					
GN Name=CD4;					
OS Macaca mulatta (Rhesus macaque)					
OC Eukaryota; Metzcoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Cercopithecoidea; Macaca.					
NCBI TAXID=9544;					
RN [1]					
RP					
SEQUENCE FROM N.A.					
RK MEDLINE=90182664; PubMed=2107024; DOI=10.1016/0092-8674(90)90089-W;					
RA Camerini D.; Seid B.;					
RA "A CD4 domain important for HIV-mediated syncytium formation lies outside the virus binding site.";					
RT Cell 60:747-754(1990).					
RN [2]					
RP					
SEQUENCE FROM N.A.					
RC Tissue:Thymocytes;					
RA Hashimoto O., Tatsumi M.;					
RT "Molecular cloning and expression of macaque CD4B";					
RT Submitted (UN-1995) to the EMBL/GenBank/DBJ databases.					
RN [3]					

RP	SEQUENCE OF 28-424 FROM N.A.
RC	TISSUE=BLOOD;
MEDLINE=93049640; PubMed=1425921;	
RA	Fomsgaard A., Hirach V.M., Johnson P.R.;
RT	"Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus"; 2981(1992).
RT	EUR. J. Immunol. 22:2973-2981(1992).
RL	[4]
RN	SEQUENCE OF 107-192 FROM N.A.
RP	MDLINE=98320644; PubMed=9856488;
RA	Harris E.E., Disatelli T.R.;
RT	"Nuclear gene trees and the phylogenetic relationships of the mangabey (Primates: Papionini)"; Mol. Biol. Evol. 15:892-900(1998).
RL	-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
CC	-I- SUBUNIT: Associates with p56-lick (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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EMBL; M31134; AA036838.1; -.	
EMBL; D63347; BAA09671.1; -.	
EMBL; AF053385; AAC25129.1; -.	
DR	HSSP; P01710; IWR.
DR	GO; 001526; C-T-cell receptor complex; ISS.
DR	GO; 002101; C-T-cell receptor activity; ISS.
DR	GO; 0042289; P:MHC class II protein binding; ISS.
DR	GO; 0045086; P:positive regulation of interleukin-2 biosyn. . . ; ISS.
DR	GO; 0045087; P:T-cell differentiation; ISS.
DR	GO; 0017169; P:transmembrane receptor protein tyrosine kin. . . ; ISS.
DR	InterPro; IPR008424; CD2.
DR	InterPro; IPR00973; CD4_Tcag.
DR	InterPro; IPR01710; Ig-Tire.
DR	InterPro; IPR03596; Ig_V.
DR	Pfam; PF00047; Ig_2.
DR	PRINTS; PR00692; CD4TCANTIGEN.
DR	SMART; SM00406; Ig_V.
DR	PROSITE; PS50835; Ig_LIKE_1.
KW	Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; Palmitate; Repeat; Signal; T-cell; Transmembrane.
FT	CHAIN
FT	26 458
FT	DOMAIN 26 396
FT	TRANSMEM 397 418
FT	DOMAIN 419 458
FT	DOMAIN 26 125
FT	DOMAIN 126 203
FT	DOMAIN 204 317
FT	DOMAIN 318 374
FT	CARBHD 296 295
FT	CARBHD 325 325
FT	DISULFID 41 109
FT	DISULFID 155 184
FT	DISULFID 328 370
FT	LIPID 419 419
FT	LIPID 422 422
FT	CONFFLICT 42 42
FT	CONFFLICT 62 62
FT	CONFFLICT 67 67
FT	CONFFLICT 169 169
RESULT 5	
CD4_MACFA	CD4_MACFA
ID	STANDARD;
AC	P79785;
DT	15-JUL-1998 (Rel. 36, last sequence update)
DT	05-JUL-2004 (Rel. 44, last annotation update)
DB	T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/leu-3).
DR	Name=CD4;
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC	Cercopithecinae; Macaca.
OX	NCBI_TaxID=9541;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Thymocytes;
RA	Tatsumi M., Yabe M., Yamada Y.K.;
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC	-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
CC	-I- SUBUNIT: Associates with p56-lick (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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PT CARBOHYD 42 42 N-linked (GlcNAc. . .) (Potential).
 PT CARBOHYD 296 296 N-linked (GlcNAc. . .) (By similarity).
 PT CARBOHYD 325 325 N-linked (GlcNAc. . .) (By similarity).
 PT DISULFID 41 109 By similarity.
 PT DISULFID 155 184 By similarity.
 PT DISULFID 328 370 By similarity.
 PT LIPID 419 419 S-palmitoyl cysteine (By similarity).
 PT LIPID 422 422 S-palmitoyl cysteine (By similarity).
 PT LIPID 57 57 D -> N (in Ref. 2).
 PT CONFLICT 91 91 C -> H (in Ref. 2).
 PT CONFLICT 105 105 N -> D (in Ref. 2).
 PT CONFLICT 113 113 N -> D (in Ref. 2).
 PT CONFLICT 302 302 D -> E (in Ref. 2).
 PT CONFLICT 349 349 D -> E (in Ref. 2).
 PT SEQUENCE 458 AA; T -> A (in Ref. 2).
 SQ SEQUENCE 5095 MW: 75198BA2CB3EE16 CRC64;

Query Match 90.4%; Score 1835; DB 1; Length 458;
 Best Local Similarity 89.8%; Pred. No. 4; e-16; Mismatches 21; Indels 0; Gaps 0;
 Matches 354; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MNRGVPRHLVLTQVQLLPAATQGNKWLAKRGKPTVELTCASOKKSIQHFKNSNOIK 60
 Db 1 MNRGIPPRHLVLTQVQLLPAATQGNKWLAKRGKPTVELTCASOKKSIQHFKNSNOIK 60
 Qy 61 ILGNQCSPLTKPSKSKUNDRANSRSUIMQDGIPPLIKNLKEEDSDTYCIEFDQKEVOL 120
 Db 61 ILGQCSPLTKPSKSKUNDRANSRSUIMQDGIPPLIKNLKEEDSDTYCIEFDQKEVOL 120
 Qy 121 LVFGLTANSDTILQGQSLTTLSPPGSSVQCSPRGKNIQGGKTLSVQLEQDGS 180
 Db 121 LVFGLTANSDTILQGQSLTTLSPPGSSVQCSPRGKNIQGGKTLSVQLEQDGS 180
 Qy 181 TWCTCTVQKVKERKIDIVVIAFQKASSIVKKEQSVRSPPLAFTVEKLTGSEBLW 240
 Db 181 TWCTCTVQKVKERKIDIVVIAFQKASSIVKKEQSVRSPPLAFTVEKLTGSEBLW 240
 Qy 301 LDAKIGKLHQEVNLVVRATQDQKLNLTCEVNGPSPKLMISLXLENKEAKVSSREKVV 360
 Db 301 LDAKIGKLHQEVNLVVRATQDQKLNLTCEVNGPSPKLMISLXLENKEAKVSSREKVV 360
 Qy 361 LPNEAGWQCLISDSCGYLSSNIKVLPTWSPV 394
 Db 361 LPNEAGWQCLISDSCGYLSSNIKVLPTWSPV 394

RESULT 7

CD4_CERAE STANDARD; PRT; 458 AA.

AC Q008378; O02805; O77593; Q28217; DT 0-FEB-1995 (Rel. 31; Created)
 DT 29-MAR-2004 (Rel. 43; Last sequence update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3').
 DE Name:CD4; Pfam: PF00047; ig; 2.
 OS Cercopithecus aethiops (green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Cercopithecidae; Cercopithecus.
 OC [1] NCBI_TaxID=9534;
 RN SEQUENCE FROM N.A.
 RP Hashimoto O.; Tatsumi M.; "Molecular cloning and expression of african green monkey CD4.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2] SEQUENCE OF 28-424 FROM N.A.
 RP TISSUE=Blood;
 RX MEDLINE=93049640; PubMed=1425921;

RJ Fomsgaard A.; Hirsch V.M.; Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus."; Eur. J. Immunol. 22:2973-2981(1992).
 RJ [3] SEQUENCE OF 28-424 FROM N.A.
 RP TISSUE=Peripheral blood;
 RC MEDLINE=98017879; PubMed=9379478;
 RA Fomsgaard A.; Mueller-Trutwin M.C.; Diop O.; Hansen J.; Mathiot C.; Corbet S.; Barre-Sinoussi F.; Allan J.S.; "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes."; J. Med. Primatol. 26:120-128(1997).
 RN SEQUENCE OF 107-192 FROM N.A.
 RA MEDLINE=98320644; PubMed=9656488;
 RA Harris E.B.; Discott T.R.; "Nuclear gene trees and the phylogenetic relationships of the mangabeys (Primates: Papionini)." Mol. Biol. Evol. 15:892-900(1998).
 CC -I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
 CC -I- SUBUNIT: Accesses with P56-ICK (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to licensee@isb-sib.ch).
 CC
 DR EMBL; D8589; BRA13132.1; -.
 DR EMBL; X73322; CHAR1748.1; -.
 DR EMBL; AF001226; AAB80873.1; -.
 DR EMBL; AF001228; AAB80875.1; -.
 DR EMBL; AF057380; AAC25124.1; -.
 DR HSSP; P01730; IWTQ.
 DR GO; GO:0042101; C-T-cell receptor complex; ISS.
 DR GO; GO:0015026; F:coreceptor activity; ISS.
 DR GO; GO:006955; P:immune response; ISS.
 DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
 DR GO; GO:003217; P:T-cell differentiation; ISS.
 DR GO; GO:0045058; P:T-cell selection; ISS.
 DR GO; GO:0001169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
 DR InterPro; IPR008424; CD2.
 DR InterPro; IPR007110; Ig-Tike.
 DR Pfam; PF00047; ig; 2.
 DR PRINTS; PR00692; CD4TCANTIGEN.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
 PT SIGNAL 1 25 By similarity.
 PT CHAIN 26 458 T-cell surface glycoprotein CD4.
 PT DOMAIN 25 396 Extracellular (Potential).
 PT DOMAIN 397 418 Potential.
 PT TRANSMEM 419 458 Cytoplasmic (Potential).
 PT DOMAIN 26 125 Ig-like V-type.
 PT DOMAIN 126 203 Ig-like C2-type 1.
 PT DOMAIN 204 317 Ig-like C2-type 2.
 PT DOMAIN 318 374 Ig-like C2-type 3.
 PT CARBOHYD 42 42 N-linked (GlcNAc. . .) (Potential).
 PT CARBOHYD 281 281 N-linked (GlcNAc. . .) (Potential).
 PT CARBOHYD 296 296 N-linked (GlcNAc. . .) (Potential).
 PT CARBOHYD 325 325 N-linked (GlcNAc. . .) (Potential).
 PT DISULFID 41 109 By similarity.
 PT DISULFID 155 184 By similarity.

Qy	328	CEWGPSPKULSLKLENKEAKVSKRKPVNTLNPERAGMWCILSPSGQVILESNIKV	387	DOMAIN	392	>397	Cytoplasmic (Potential).
Db	301	CEWGPSPKULSLKLENKEAKVSKRKPVNTLNPERAGMWCILSPSGQVILESNIKV	360	DOMAIN	<1	98	Ig-like V-type.
Qy	388	PTWSTPV	394	DOMAIN	99	176	Ig-like C2-type 1.
Db	361	PTWSTPV	367	DOMAIN	177	290	Ig-like C2-type 2.
RESULT 9							
ID	CD4_CERTO	STANDARD	PRT;	PRT;	397 AA.		
AC	008336;						
DT	01-OCT-1996 (Rel. 34. Last sequence update)						
DT	05-JUL-2004 (Rel. 44. Last annotation update)						
DE	T-cell surface glycoprotein CD4 (T-cell surface antigen T4/leu-3) (Fragment).						
DB	Name=cCD4;						
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).						
OC	BukarYota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;						
OX	NCBI_TaxID=9531;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Blood;						
RX	Pomgaard A., Hirsch V.M., Johnsen P.R.;						
RA	PMID=93049640; PubMed=1425921;						
RT	"Cloning and sequence of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus."						
RT	Bur. J. Immunol. 22:2973-2981(1992).						
CC	-!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.						
CC	-!- SUBUNIT: Associates with p56-ICK (By similarity).						
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.						
CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.						
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.ebi-sib.ch/announce/ or send an email to license@ebi-sib.ch).						
CC	EMBL; X73328; CAAS1754.1; -.						
DR	EMBL; X73327; CAAS1753.1; -.						
DR	HSSP; P01730; IWIQ.						
DR	GO; GO:0042101; C:T-cell receptor complex; ISS.						
DR	GO; GO:0015026; F:co-receptor activity; ISS.						
DR	GO; GO:0015026; F:co-receptor complex; ISS.						
DR	GO; GO:0042289; P:MHC class II protein binding; ISS.						
DR	GO; GO:006955; P:immune response; ISS.						
DR	GO; GO:0015086; P:positive regulation of interleukin-2 biosyn. . . ; ISS.						
DR	GO; GO:0032017; P:T-cell differentiation; ISS.						
DR	GO; GO:0045058; P:T-cell selection; ISS.						
DR	GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; ISS.						
DR	InterPro; IPR008424; CD2.						
DR	InterPro; IPR000973; CD4_TCAG.						
DR	InterPro; IPR007110; Ig-like.						
DR	InterPro; IPR003596; Ig_V.						
DR	PRINTS; PR00047; Ig; 2.						
DR	PRINTS; PR00692; CD4_CANTIGEN.						
DR	SMART; SM00406; IgV; 1.						
DR	PROSITE; PS50835; Ig_LIKE; 1.						
DR	Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;						
KW	Palmitate; Repeat; T-cell; Transmembrane.						
FT	NON_TER						
FT	DOMAIN <1						
FT	TRANSMEM 369						
FT	391 Potential.						
RA	SEQUENCE FROM N.A.						
RA	PMID=9801789; PubMed=9379478;						
RESULT 10							
DB	009261	PRELIMINARY	PRT;	PRT;	397 AA.		
AC	009261						
DT	01-JUL-1997 (T-EMBLrel. 04. Last sequence update)						
DT	01-OCT-2003 (T-EMBLrel. 25. Last annotation update)						
DB	CD4 (Fragment).						
GN	Name=cCD4;						
OS	Cercopithecus sabaeus.						
OC	Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;						
OC	Cercopithecinae; Cercopithecus.						
OX	NCBI_TaxID=60711;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	PMID=9801789; PubMed=9379478;						
RA	Pomgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,						

RA Corbet S., Barre-Sinoussi F., Allan J.S.: African green monkey CD4 genes and "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes."; J. Med. Primatol. 26:120-128 (1997).

RT J. Med. Primatol. 26:120-128 (1997).

RL EMBL; AF01225; AAB60871.1; -.

DR HSSP; P01730; IWIQ.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR008424; CD2.

DR InterPro; IPR007110; IWIQ.

DR InterPro; IPR007110; Ig-Tike.

DR InterPro; IPR003596; Ig V.

DR Pfam; PF05790; C2-set; 2.

DR Pfam; PF0047; Ig; 1.

DR PRINTS; PRO0692; CD4CANTIGEN.

DR SMART; SM0406; IgV; 1.

DR PROSITE; PS50835; Ig-LIKE; 1.

FT FT NON_TER 397 AA; 43945 MW; 80C963B92A868CD3 CRC64;

SQ SEQUENCE 397 AA; 397 AA; 397 AA; 43882 MW; 478BB277E92E89 CRC64;

Query Match 84.0%; Score 1705; DB 2; Length 397; Best Local Similarity 89.9%; Pred. No. 1.2e-116; Mismatches 15; Indels 22; Gaps 0; Gaps 0; Matches 330; Conservative

QY 28 VVLGKKGDTVELCTASOKS1OPHWKNSNQ1KLGNOGSFTKGSKLNRADRSRSLW 87

Db 1 VVLGKKGDTVELCTASOKS1OPHWKNSNQ1KLGNOGSFTKGSKLNRADRSRSLW 60

QY 88 DQGNPLIPLKNIKLEDSPVYCEVEDKEVOLVFGILTANSDTLHQGOSTTLESP 147

Db 61 DQGCSMIIKNIKLEDSPVYCEVENKEVOLVFGILTANSDTLHQGOSTTLESP 120

QY 148 GSSPSVQCSPRGKNIQSKTLVSQSLQDQSGTWCTVLOQKVKVERKIDIVLAQKA 207

Db 121 GSSPSVQCSPRGKNIQGRTLSVPOLERQDGTWTCTVLOQKVKVERKIDIVLAQKA 180

Db 208 SSVIKKEGQVERSPFLAFTVEKLTKGSELIWQAEARISSKSWITFDLKNEVSVRT 267

QY 241 QDPKLUQMGKPLNITLTPQALPOVAGSGNLTAEAKTGKHLQEVNLVNRATQFOENLT 300

Db 181 SSVIKKEGQVERSPFLAFTVEKLTKGSELIWQAEARISSKSWITFDLKNEVSVRT 240

QY 268 QDPKLUQMGKPLNITLTPQALPOVAGSGNLTAEAKTGKHLQEVNLVNRATQFOENLT 327

Db 241 QDPKLUQMGKPLNITLTPQALPOVAGSGNLTAEAKTGKHLQEVNLVNRATQFOENLT 300

QY 328 CEWGWGTPSKMLSIKLENKATVQAKSKREKPVWVNLPEAGMWQCLSDSQVILLESNIKL 387

Db 301 CEWGWGTPSKMLSIKLENKATVQAKSKREKPVWVNLPEAGMWQCLSDSQVILLESNIKL 360

QY 388 PWSTPV 394

Db 361 PWTPTPV 367

RESULT 11

009250 PRELIMINARY; PRT; 397 AA.

ID 009260 PRELIMINARY; PRT; 397 AA.

AC 009260; 01-JUL-1997 (TREMBREL. 04, Created)

DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DR (Fragment).

GN Name=CD4;

OS Cercopithecus sabaeus.

OC Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopithecinae; Cercopithecidae.

OC Cercopithecinae; Cercopithecidae.

NCBI NCBI_TaxID=60711;

RN [1]

SEQUENCE FROM N.A. MEDLINE=98017879; PubMed=9379478; RX Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., RA

RA Corbet S., Barre-Sinoussi F., Allan J.S.; "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes."; J. Med. Primatol. 26:120-128 (1997).

RT J. Med. Primatol. 26:120-128 (1997).

RL EMBL; AF01224; AAB60871.1; -.

DR HSSP; P01730; IWIQ.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR008424; CD2.

DR InterPro; IPR007110; CD4 TCAG.

DR InterPro; IPR007110; Ig-Tike.

DR InterPro; IPR003596; Ig V.

DR Pfam; PF05790; C2-set; 2.

DR Pfam; PF0047; Ig; 1.

DR PRINTS; PRO0692; CD4CANTIGEN.

DR SMART; SM0406; IgV; 1.

DR PROSITE; PS50835; Ig-LIKE; 1.

FT FT NON_TER 397 AA; 397 AA; 397 AA; 43882 MW; 478BB277E92E89 CRC64;

SQ SEQUENCE 397 AA; 397 AA; 397 AA; 43882 MW; 478BB277E92E89 CRC64;

Query Match 83.8%; Score 1701; DB 2; Length 397; Best Local Similarity 89.8%; Pred. No. 2.4e-16; Mismatches 16; Indels 22; Gaps 0; Gaps 0; Matches 329; Conservative

QY 28 VVLGKKGDTVELCTASOKS1OPHWKNSNQ1KLGNOGSFTKGSKLNRADRSRSLW 87

Db 1 VVLGKKGDTVELCTASOKS1OPHWKNSNQ1KLGNOGSFTKGSKLNRADRSRSLW 60

QY 88 DQGNPLIPLKNIKLEDSPVYCEVEDKEVOLVFGILTANSDTLHQGOSTTLESP 147

Db 61 DQGCSMIIKNIKLEDSPVYCEVENKEVOLVFGILTANSDTLHQGOSTTLESP 120

QY 148 GSSPSVQCSPRGKNIQSKTLVSQSLQDQSGTWCTVLOQKVKVERKIDIVLAQKA 207

Db 121 GSSPSVQCSPRGKNIQGRTLSVPOLERQDGTWTCTVLOQKVKVERKIDIVLAQKA 180

Db 208 SSVIKKEGQVERSPFLAFTVEKLTKGSELIWQAEARISSKSWITFDLKNEVSVRT 267

QY 241 QDPKLUQMGKPLNITLTPQALPOVAGSGNLTAEAKTGKHLQEVNLVNRATQFOENLT 300

Db 181 SSVIKKEGQVERSPFLAFTVEKLTKGSELIWQAEARISSKSWITFDLKNEVSVRT 240

QY 268 QDPKLUQMGKPLNITLTPQALPOVAGSGNLTAEAKTGKHLQEVNLVNRATQFOENLT 327

Db 241 QDPKLUQMGKPLNITLTPQALPOVAGSGNLTAEAKTGKHLQEVNLVNRATQFOENLT 300

QY 328 CEWGWGTPSKMLSIKLENKATVQAKSKREKPVWVNLPEAGMWQCLSDSQVILLESNIKL 387

Db 301 CEWGWGTPSKMLSIKLENKATVQAKSKREKPVWVNLPEAGMWQCLSDSQVILLESNIKL 360

QY 388 PWSTPV 394

Db 361 PWTPTPV 367

RESULT 12

009250 PRELIMINARY; PRT; 397 AA.

ID 009260 PRELIMINARY; PRT; 397 AA.

AC 009260; 01-DEC-2001 (TREMBREL. 19, Created)

DT 01-DEC-2001 (TREMBREL. 19, Last sequence update)

DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)

DE CD4 (Fragment).

GN Name=CD4;

OS Cercopithecus pygerythrus (Vervet monkey).

OC Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Cercopithecinae; Cercopithecidae.

OC Butheria; Primates; Catarhini; Cercopithecidae.

NCBI NCBI_TaxID=60711;

RN [1]

SEQUENCE FROM N.A. MEDLINE=98017879; PubMed=9379478; RX Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., RA

RA Corbet S., Barre-Sinoussi F., Allan J.S.;
 RT "Relation between phylogeny of African green monkey CD4 genes and
 their respective simian immunodeficiency virus genes.";
 RL J. Med. Primatol. 26:120-128(1997).
 EMBL: AF00227; AAB60874.1; -.
 DR HSSP: P01730; IWIQ.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0007155; P:cell adhesion; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR008424; CD2.
 DR InterPro: IPR000973; CD4 TCAG.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF05790; C2-set; 2.
 DR PRINTS: PR00692; CD4TCANTIGEN.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; Ig_LIKE; 1.
 PT NON_TER 1
 FT NON_TER 397 AA; 397 MW; 21C3B30882ABFBC0 CRC64;
 SQ SEQUENCE 397 AA; 43946 MW; 21C3B30882ABFBC0 CRC64:

Query Match 83.8%; Score 1700; DB 2; Length 397;
 Best Local Similarity 89.6%; Pred. No. 2-8e-116; Mismatches 15; Indels 0; Gaps 0;
 Matches 329; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

Qy 28 VVLGKKGDTVLLTCTASOKSIQFHWNNSNOKILKNGNQSGFTTKGSKLNDRDRSLW 87
 Db 1 VVLGKKGDTVLLTCTASOKSIQFHWNNSNOKILKNGNQSGFTTKGSKLNDRDRSLW 60

Qy 88 DQGNPLIKIKLIEDSDTICVEQDQEKEVQVLLVGLTANSDTIHLQGSLTLESPP 147
 Db 61 DQGCFSMIKLNIKIEDSETVYCEVENKEEVLLVGLTANSDTIHLQGSLTLESPP 120

Qy 148 GSSPSVQCRSPRGKNIQGGKTLVSQLEQDLSGNTCTVILQNKKEFKIDIVVLAQKA 207
 Db 121 GSSPSVQCRSPRGKNIQGGKTLVSQLEQDLSGNTCTVILQNKKEFKIDIVVLAQKA 180

Qy 208 SSIVYKKGEGOEVFSPLAFTVEKLTGSGELWWQABRASSSKSWITPDLNKEVSKVRT 267
 Db 181 SSTVYKKGEGOEVFSPLAFTLEKLTGSGELWWQABRASSSKSWITPDLNKEVSKVQT 240

Qy 268 QDPKLGQMKKPLHLLTLPQALPOQYAGSGNLTALRAKTKQHQEVLNLVWRAQTLQKNLT 327
 Db 241 QDPKLGQMKKPLHLLTLPQALPOQYAGSGNLTALRAKTKQHQEVLNLVWRAQTLQKNLT 300

Qy 328 CEVWGTSPKUMLSKLENEKAVSKRKPWVNLNPEAGWQCLLSDSGQVLESNIKV 387
 Db 301 CEVWGTSPKUMLSKLENEKAVSKRKPWVNLNPEAGWQCLLSDSGQVLESNIKV 360

Qy 388 PTWSTPV 394
 Db 361 PTWPTPV 367

RESULT 13

009259 PRELIMINARY; PRT; 397 AA.

ID 009259; PRELIMINARY; PRT; 397 AA.

AC 009259; PRELIMINARY; PRT; 397 AA.

DT 01-JUL-1997 (TrEMBLrel. 04, last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)

DB CD4 (Fragment).

GN Name=CD4;

OS Cercopithecus babaens.

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Cercopithecus; NCBI_TaxID=60711;

RN [1]

RP SEQUENCE FROM N.A. MEDLINE=90017879; PubMed=9379478;

RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,

RESULT 14

009263 PRELIMINARY; PRT; 397 AA.

ID 009263 PRELIMINARY; PRT; 397 AA.

AC 009263; PRELIMINARY; PRT; 397 AA.

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DB CD4 (Fragment).

GN Name=CD4;

OS Cercopithecus tantalus.

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Cercopithecus; NCBI_TaxID=60712;

RN [1]

RP SEQUENCE FROM N.A. MEDLINE=90017879; PubMed=9379478;

RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,

RA Corbet S., Barre-Sinoussi F., Allan J.S.; "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes."; J. Med. Primatol. 26:120-128(1997).

RT EMBL; AF001222; AAB60869.1; -.

RT HSSP; P01730; IWIQ.

RT GO; GO:0016021; C: integral to membrane; IEA.

RT GO; GO:0007155; P: cell adhesion; IEA.

RT GO; GO:0006955; P: immune response; IEA.

RT InterPro; IPR008424; CD2.

RT InterPro; IPR00973; CD4 TCAG.

RT InterPro; IPR007110; Ig-like.

RT InterPro; IPR003596; Ig v.

RT Pfam; PF05790; C2-set; 2.

RT DR PRINTS; PR00692; CD4TCANTIGEN.

RT SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; Ig-LIKE; 1.

FT NON-TER 1

FT NON-TER 397 AA; 43994 MW; A3CD031535A51524 CRC64;

Query Match 83.6%; Score 1696; DB 2; Length 397; Best Local Similarity 89.4%; Pred. No. 5.e-116; Mismatches 15; Indels 24; Gaps 0; Matches 328; Conservative 15; Mismatches 24; Indels 0; Gaps 0; Sequence 397 AA; 43994 MW; A3CD031535A51524 CRC64;

Query Match 83.2%; Score 1699; DB 2; Length 397; Best Local Similarity 89.4%; Pred. No. 1.8e-115; Mismatches 15; Indels 24; Gaps 0; Matches 328; Conservative 15; Mismatches 24; Indels 0; Gaps 0; Sequence 397 AA; 43954 MW; CF7F2F5D82335B0D CRC64;

Query Match 83.2%; Score 1699; DB 2; Length 397; Best Local Similarity 89.4%; Pred. No. 1.8e-115; Mismatches 15; Indels 24; Gaps 0; Matches 328; Conservative 15; Mismatches 24; Indels 0; Gaps 0; Sequence 397 AA; 43954 MW; CF7F2F5D82335B0D CRC64;

QY 28 VVLGKKGDTPVELTCTASOKKSIQFHWNNSNQIKILGNQSGPLTKPSKLNDRADRSRSLW 87

Db 1 VVLGKKGDTPVELTCTASQNTTQFHWNNSNQIKILGKQSGFIFTKGSSKLDRDRDSRSLW 60

QY 88 DQGNFLIPIKNUKIEDSDTYCERDVEQKEVQVOLVGLTANSDDHILQGSLTTLQESPP 147

Db 61 DQGCFSMIKNUKIEDSETYCEVENKEVELVLFGLTANSDDHILQGSLTTLQESPP 120

QY 148 GSSPSVQCRSPRGKNIQGKTKLVSQLEQIQLDQSGTWTCTLQONQKKEFKDIDIVLAFOKA 207

Db 121 GSSPSVCRSPRGKNIQGKTKLVSQLEQIQLDQSGTWTCTLQONQKKEFKDIDIVLAFOKA 180

QY 208 SSVIYKKEGEOVESPFLAFTVEKLTGSGELWQAEERASSSSWITPDLKRNKEVSKVKT 267

QY 181 SSVIYKKEGEOVESPFLAFTLEKLTGSGELWQAEERASSSSWITPDLKRNKEVSKVKT 240

QY 268 QDPKLOMGKKPLHILTLPOALPOAGSGNLTIALEAKTGHQEVNLVWRAATQOLNLT 327

Db 241 QDPKLOMGKKPLHILTLPOALPOAGSGNLTIALEAKTGHQEVNLVWRAATQOLNLT 300

QY 328 CSEWGGPTSPKLMISLKLLENKEAKVSKREKPVWLNPEAGMOCILSDSGQVILLESNIKV 387

Db 301 CSEWGGPTSPKLMISLKLLENKAATVSKQAKAVWLNPEEGMMOCILSDSGQVILLESNIKV 360

QY 388 PTWSTPV 394

Db 361 PTWSTPV 367

RESULT 15

009262 PRELIMINARY; PRT; 397 AA.

ID 009262;

AC 009262; "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes."; J. Med. Primatol. 26:120-128(1997).

DT 01-JUL-1997 (TREMBrel. 04, Created)

DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)

DE CD4 (Fragment).

GN Name-CD4;

OS Cercopithecus tantalus.

OC Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Cercopithecus.

OC NCBI_TAXID=60712;

RN [1]

RP SEQUENCE FROM N_A.

RX MEDLINE=98017879; PubMed=9379478;

RA Romsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,

Search completed: March 7, 2005, 07:19:30
Job time : 151.542 secs